(FILE 'HOME' ENTERED AT 10:40:17 ON 13 JUL 2003

FILE 'REGISTRY' ENTERED AT 10:40:30 ON 13 JUL 2003
L1 44 S CC.{4}C.Y.C/SQSP

FILE 'CA' ENTERED AT 10:44:44 ON 16 JUL 2003
L2 25 S L1
L3 5 S CONOTOXIN AND L2

L2 ANSWER 1 OF 25 CA COPYRIGHT 2003 ACS
TI Human colon and colon cancer-associated polynucleotides and polypeptides and their diagnostic and therapeutic applications
PY 2003
2001
2003

L2 ANSWER 2 OF 25 CA COPYRIGHT 2003 ACS
TI DNA and protein sequences of human hair keratin-associated proteins and their used
PY 2003

L2 ANSWER 3 OF 25 CA COPYRIGHT 2003 ACS
TI Polymorphisms in the human high sulfur hair keratin-associated protein 1, KAP1, gene family
PY 2002

L2 ANSWER 4 OF 25 CA COPYRIGHT 2003 ACS
TI Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
PY 2002

L2 ANSWER 5 OF 25 CA COPYRIGHT 2003 ACS
TI Novel conotoxins for use in the therapeutic regulation of ion channel function
PY 2002
2003
2003

L2 ANSWER 6 OF 25 CA COPYRIGHT 2003 ACS
TI Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells
PY 2002

L2 ANSWER 7 OF 25 CA COPYRIGHT 2003 ACS
TI Nucleic acids and their encoded polypeptides from human tissues
PY 2001
2001

L2 ANSWER 8 OF 25 CA COPYRIGHT 2003 ACS
TI Human nucleic acids and polypeptides and their diagnostic and therapeutic uses
PY 2001
2001
2002
2002

L2 ANSWER 9 OF 25 CA COPYRIGHT 2003 ACS
TI Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes
PY 2001
2001
2003

L2 ANSWER 10 OF 25 CA COPYRIGHT 2003 ACS
TI Complete genome sequence of the shrimp white spot bacilliform virus
PY 2001

L2 ANSWER 11 OF 25 CA COPYRIGHT 2003 ACS
TI New members of the .mu.-conotoxin family for use in the treatment of disease associated with sodium channel function and cDNAs encoding them
PY 2002
2002
2003

L2 ANSWER 12 OF 25 CA COPYRIGHT 2003 ACS
TI Characterization of a cluster of human high/ultrahigh sulfur keratin-associated protein genes embedded in the type I keratin gene domain on chromosome 17q12-21
PY 2001

L2 ANSWER 13 OF 25 CA COPYRIGHT 2003 ACS
TI Nucleic acids and their encoded [redacted]eptides from human tissues
PY 2001

L2 ANSWER 14 OF 25 CA COPYRIGHT 2003 ACS
TI Mechanisms for evolving hypervariability: the case of conopeptides
PY 2001

L2 ANSWER 15 OF 25 CA COPYRIGHT 2003 ACS
TI An efficient synthetic scheme for natural .alpha.-conotoxins and their analogues
PY 2001

L2 ANSWER 16 OF 25 CA COPYRIGHT 2003 ACS
TI Colon and colon cancer associated cDNAs and proteins and their use in diagnosis and treatment of colon cancer
PY 2001
2001
2002
2003
2003

L2 ANSWER 17 OF 25 CA COPYRIGHT 2003 ACS
TI Functional annotation of a full-length mouse cDNA collection
PY 2001

L2 ANSWER 18 OF 25 CA COPYRIGHT 2003 ACS
TI Alpha-conotoxins and nucleic acids encoding them
PY 2000
2001
2002

L2 ANSWER 19 OF 25 CA COPYRIGHT 2003 ACS
TI Human and murine secreted proteins and nucleic acids encoding them
PY 2000
2001

L2 ANSWER 20 OF 25 CA COPYRIGHT 2003 ACS
TI The genome sequence of Drosophila melanogaster
PY 2000

L2 ANSWER 21 OF 25 CA COPYRIGHT 2003 ACS
TI Cloning of human epidermal proteins HEPI-1 to HEPI-6 and their cDNA sequences and diagnostic and therapeutic applications
PY 2000
2000
2000
2000
2001
2003

L2 ANSWER 22 OF 25 CA COPYRIGHT 2003 ACS
TI RNA editing in the free-living bodonid Bodo saltans. [Erratum to document cited in CA129:1279]
PY 1998

L2 ANSWER 23 OF 25 CA COPYRIGHT 2003 ACS
TI RNA editing in the free-living bodonid Bodo saltans
PY 1998

L2 ANSWER 24 OF 25 CA COPYRIGHT 2003 ACS
TI Structure and hair follicle-specific expression of genes encoding the rat high sulfur protein B2 family
PY 1998

L2 ANSWER 25 OF 25 CA COPYRIGHT 2003 ACS
TI Cloning and structural characterization of human hair high-sulfur keratin genes
PY 1992

ANSWER 1 OF 5 CA COPYRIGHT 2003 ACS
TI Novel conotoxins for use in the therapeutic regulation of ion channel function
PY 2002
2003
2003

L3 ANSWER 2 OF 5 CA COPYRIGHT 2003 ACS
TI New members of the .mu.- ***conotoxin*** family for use in the treatment of disease associated with sodium channel function and cDNAs encoding them
PY 2002

2002
2003

L3 ANSWER 3 OF 5 CA COPYRIGHT 2003 ACS
TI Mechanisms for evolving hypervariability: the case of conopeptides
PY 2001

L3 ANSWER 4 OF 5 CA COPYRIGHT 2003 ACS
TI An efficient synthetic scheme for natural .alpha.-conotoxins and their analogues
PY 2001

L3 ANSWER 5 OF 5 CA COPYRIGHT 2003 ACS
TI Alpha-conotoxins and nucleic acids encoding them
PY 2000
2001
2002

L4 ANSWER 1 OF 1 CA COPYRIGHT 2003 ACS
AN 119:87666 CA
TI Cloning and structural characterization of human hair high-sulfur keratin genes
AU Zhumabaeva, B. D.; Gening, L. V.; Gazaryan, K. G.
CS Inst. Mol. Genet., Moscow, 123182, Russia
SO Molekulyarnaya Biologiya (Moscow) (1992), 26(4), 813-20
CODEN: MOBIBO; ISSN: 0026-8984
DT Journal
LA Russian

L2 ANSWER 23 OF 25 CA COPYRIGHT 2003 ACS
AN 129:1279 CA
TI RNA editing in the free-living bodonid Bodo saltans
AU Blom, Daniel; De Haan, Annett; Van Den Berg, Marlene; Sloof, Paul; Jirku, Milan; Lukes, Julius; Benne, Rob
CS Department of Biochemistry/AMC, University of Amsterdam, Amsterdam, 1105 AZ, Neth.
SO Nucleic Acids Research (1998), 205-1213
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB In parasitic kinetoplastid protozoa, mitochondrial (mt) mRNAs are post-transcriptionally edited by insertion and deletion of uridylate residues, the information being provided by guide (g) RNAs. In order to further explore the role and evolutionary history of this process, we searched for editing in mt RNAs of the free-living bodonid Bodo saltans. We found extensive editing in the transcript for NADH dehydrogenase (ND) subunit 5, which is unedited in trypanosomatids. In contrast, B. saltans cytochrome c oxidase (cox) subunit 2 and maxicircle unidentified reading frame (MURF) 2 RNAs display limited editing in the same regions as their trypanosomatid counterparts. A putative intramol. cox2 gRNA and the gene for gMURF2-1 directing the insertion of only one U in the 5' editing domain of MURF2 RNA, are conserved in B. saltans. This lends (further) evolutionary support to the proposed role of these sequences as gRNAs. Phylogenetic anal. showed that B.saltans is more closely related to trypanosomatids than the cryptobiids Trypanoplasma borreli and Cryptobia helicis, in line with the trypanosomatid-like cox2 and MURF2 RNA editing patterns. Nevertheless, other features like the apparent absence of a catenated mtDNA network, are shared with bodonid and cryptobiid species. ND5 RNA editing may represent yet another example of editing 'on the way out' during kinetoplastid evolution, but in view of the fact that cox2 RNA is unedited in T. borreli and C. helicis, we infer that the editing of this RNA may have arisen relatively recently. Our results provide the first examples of RNA editing in a free-living kinetoplastid, indicating that there is no direct link between U-insertion/deletion editing and a parasitic lifestyle.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 14 OF 25 CA COPYRIGHT 2003 ACS
AN 135:222087 CA
TI Mechanisms for evolving hypervariability: the case of conopeptides
AU Conticello, Silvestro G.; Gilad, Yoav; Avidan, Nili; Ben-Asher, Edna; Levy, Zehava; Fainzilber, Mike
CS Laboratory of Molecular Neurobiology, Department of Biological Chemistry, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, 76100, Israel
SO Molecular Biology and Evolution (2001), 18(2), 120-131
CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB Hypervariability is a prominent feature of large gene families that mediate interactions between organisms, such as venom-derived toxins or Igs. In order to study mechanisms for evolution of hypervariability, we examd. an EST-generated assemblage of 170 distinct conopeptide sequences from the venoms of five species of marine Conus snails. These sequences were assigned to eight gene families, defined by conserved elements in the signal domain and untranslated regions. Order-of-magnitude differences were obsd. in the expression levels of individual conopeptides, with five to seven transcripts typically comprising over 50% of the sequenced clones in a given species. The conopeptide precursor alignments revealed four striking features peculiar to the mature peptide domain: (1) an accelerated rate of nucleotide substitution, (2) a bias for transversions over transitions in nucleotide substitutions, (3) a position-specific conservation of cysteine codons within the hypervariable region, and (4) a preponderance of nonsynonymous substitutions over synonymous substitutions. We propose that the first three observations argue for a mutator mechanism targeted to mature domains in conopeptide genes, combining a protective activity specific for cysteine codons and a mutagenic polymerase that exhibits transversion bias, such as DNA polymerase V. The high Dn/Ds ratio is consistent with pos. or diversifying selection, and further analyses by intraspecific/interspecific gene tree contingency tests weakly support recent diversifying selection in the evolution of conopeptides. Since only the most highly expressed transcripts segregate in gene trees according to the feeding specificity of the species, diversifying selection might be acting primarily on these sequences. The combination of a targeted mutator mechanism to generate high variability with the subsequent action of diversifying selection on highly expressed variants might explain both the hypervariability of conopeptides and the large no. of unique sequences per species.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT